AMENDMENTS

In the Claims:

Claims 1-31. (Canceled)

32. (Previously presented) The method of claim 63, 84, 85, 88, or 106 wherein at least 50% by weight of all proteins in the sample are removed.

Claims 33-51. (Canceled)

52. (Previously presented) The method of claim 63, 84, or 85, further comprising the step of analyzing a plurality of proteins remaining in the modified sample.

Claims 53-61. (Canceled)

62. (**Currently Amended**) The method of claim 63, 84, or 85, wherein at least one of the ~~specific predefined~~ proteins is present at higher abundance than at least one of the plurality of proteins remaining in the sample after removal of the ~~specific predefined~~ proteins.

63. (**Currently Amended**) A method for **producing a modified sample** ~~separating proteins from a sample that contains proteins and recovering a modified sample for analysis of remaining proteins~~ **, said method** comprising:

removing at least a first protein and a second protein from a sample, said removing step comprising contacting said sample with an affinity binding composition comprising a first solid phase matrix with a first receptor immobilized thereon capable of specific binding to said first protein but not said second protein and a second solid phase matrix with a second receptor immobilized thereon capable of specific binding to said second protein but not said first protein, wherein each said solid phase matrix is a plurality of particles and said first and second solid phase matrices are present as a mixture in said binding composition,

~~removing at least two specific predefined ligands from a sample that contains the at least two specific predefined ligands thereby producing a modified sample containing a plurality of proteins that was present in the sample prior to removal of the at least two specific predefined ligands; and~~

~~recovering the modified sample,~~

~~wherein;~~

~~(a) the predefined ligands are proteins; and~~

~~(b) the removing step comprises contacting the sample with an affinity binding composition comprising:~~

~~a first and a second solid phase matrix contacting each other, wherein each solid phase matrix comprises a plurality of particles, and wherein the particles of the first and second solid phase matrices are present as a mixture in said affinity binding composition~~;

~~a first receptor immobilized on said first solid phase matrix, capable of specific binding to a first protein but not a second protein, and~~

~~a second receptor immobilized on said second solid phase matrix, capable of specific binding to a second protein but not the first protein,~~

so that~~,~~ when ~~the~~ **said** sample is contacted with ~~the~~ **said** affinity binding composition, **said** first protein present in ~~the~~ **said** sample binds to **said** first receptor present on ~~the~~ **said** first solid phase matrix **such that said first protein is removed from said sample** and **said** second protein present in ~~the~~ **said** sample binds to **said** second receptor present on ~~the~~ **said** second solid phase matrix such that ~~first and~~ **said** second proteins ~~are~~ **is** removed from ~~the~~ **said** sample and ~~the~~ **said** modified sample is **thereby** produced**, wherein said modified sample is not bound by a solid phase matrix; and**

recovering said modified sample.

64. (Previously presented) The method of claim 63, wherein the affinity binding composition further comprises:

a third receptor immobilized on a third solid phase matrix, capable of specific binding to a third protein but not the first protein or the second protein.

65. (Previously presented) The method of claim 64, wherein the third solid phase matrix contacts the first and second solid phase matrices.

66. (Previously presented) The method of claim 63, wherein the affinity binding composition further comprises:

a fourth receptor immobilized on a fourth solid phase matrix, capable of specific binding to a fourth protein but not the first protein, the second protein or the third protein.

67. (Previously presented) The method of claim 66, wherein the fourth solid phase matrix contacts the first, second, and third solid phase matrices.

68. (Previously presented) The method of claim 67, wherein the affinity binding composition further comprises:

a fifth receptor immobilized on a fifth solid phase matrix, capable of specific binding to a protein but not the first protein, the second protein, the third protein or the fourth protein.

69. (Previously presented) The method of claim 68, wherein the fifth solid phase matrix contacts the first, second, third, and fourth solid phase matrices.

Claims 70-83. (Canceled)

84. (**Currently Amended**) A method for **producing a modified sample** ~~separating proteins from a sample that contains proteins and recovering a modified sample for analysis of remaining proteins~~**, said method** comprising:

removing at least a first protein and a second protein from a sample, said removing step comprising contacting said sample with an affinity binding composition comprising a plurality of solid phase matrices with a plurality of receptors having different protein binding specificities immobilized thereon such that each solid phase matrix has a different protein binding specificity, wherein each said solid phase matrix is a plurality of particles and said first

and second solid phase matrices are present as a mixture in said binding composition,

~~removing at least two specific predefined ligands from a sample that contains the at least two specific predefined ligands, thereby producing a modified sample containing a plurality of proteins that was present in the sample prior to removal of the at least two specific predefined ligands; and~~

~~recovering the modified sample,~~

~~wherein;~~

~~(a) the predefined ligands are proteins: and~~

~~(b) the removing step comprises contacting the sample with an affinity binding composition comprising:~~

~~a plurality of solid phase matrices arranged such that each solid phase matrix is in contact with at least one other solid phase matrix; and~~

~~a plurality of receptors having different protein binding specificities, wherein the receptors are immobilized on the plurality of solid phase matrices such that each solid phase matrix has a different protein binding specificity, wherein each solid phase matrix comprises is a plurality of particles, and wherein the particles are, present in the affinity binding composition as a mixture,~~

so that~~,~~ when ~~the~~ **said** sample is contacted with ~~the~~ **said** affinity binding composition, ~~the~~ **said** at least two ~~specific predefined~~ protein**s** ~~ligands~~ become bound to ~~the~~ **said** affinity binding composition and **said proteins are** thereby removed from the sample such that the modified sample is produced**, wherein said modified sample is not bound by a solid phase matrix; and**

recovering said modified sample.

85. (Previously presented) The method of claim 63, or 84, wherein the sample is passed through a column containing the affinity binding composition to produce the modified sample, wherein the affinity column has a fluid inlet and a fluid outlet, and wherein the modified sample is collected at the fluid outlet.

Claims 86-87. (Canceled)

88. (**Currently Amended**) The method of claim 63, 84, or 85, wherein the receptors are antibodies or antibody fragments that specifically bind to the ~~specific, predefined~~ proteins.

89. (Previously presented) The method of claim 63, 84, or 85, wherein the receptors are recombinantly produced.

Claims 90-103. (Canceled)

104. (**Currently Amended**) The method of claim 63, 84, or 85, wherein at least one of the ~~specific predefined~~ **particular** proteins is selected from the group consisting of: immunoglobulins, albumin, transferrin, haptoglobin, α_1-antitrypsin, hemopexin, α_1-acid glycoprotein, α2 HS glycoprotein, myosin, transthyretin, α_1-antichymotrypsin, apolipoprotein AI, α_2-macroglobulin, fibrinogen, and prealbumin, and combinations thereof.

105. (**Currently Amended**) The method of claim 63, 84, or 85, wherein at least two of the ~~specific predefined~~ proteins are selected from the group consisting of: immunoglobulins, albumin, transferrin, haptoglobin, α_1-antitrypsin, hemopexin, α_1-acid glycoprotein, α2 HS glycoprotein, myosin, transthyretin, α_1-antichymotrypsin, apolipoprotein AI, α_2-macroglobulin, fibrinogen, and prealbumin.

106. (**Currently Amended**) The method of claim 63, 84, 85, or 88, wherein at least three of the ~~specific predefined~~ proteins are selected from the group consisting of: immunoglobulins, albumin, transferrin, haptoglobin, α_1-antitrypsin, hemopexin, α_1-acid glycoprotein, α2 HS glycoprotein, myosin, transthyretin, α_1-antichymotrypsin, apolipoprotein AI, α_2-macroglobulin, fibrinogen, and prealbumin.

107. (**Currently Amended**) The method of claim 63, 84, or 85, wherein at least four of the ~~specific predefined~~ proteins are selected from the group consisting of: immunoglobulins, albumin, transferrin, haptoglobin, α_1-antitrypsin, hemopexin, α_1-acid glycoprotein, α2 HS glycoprotein, myosin, transthyretin, α_1-antichymotrypsin, apolipoprotein AI, α_2-macroglobulin, fibrinogen, and prealbumin.

Claims 108 - 109. (Canceled)

110. (**Currently Amended**) The method of claim 63, wherein at least three ~~specific predefined~~ proteins are removed from a sample.

111. (**Currently Amended**) The method of claim 84, wherein at least the ~~specific predefined~~ proteins are removed from a sample,

112. (**Currently Amended**) The method of claim 63, wherein at least four ~~specific predefined~~ proteins are removed from a sample.

113. (**Currently Amended**) The method of claim 84, wherein at least four ~~specific predefined~~ proteins are removed from a sample.